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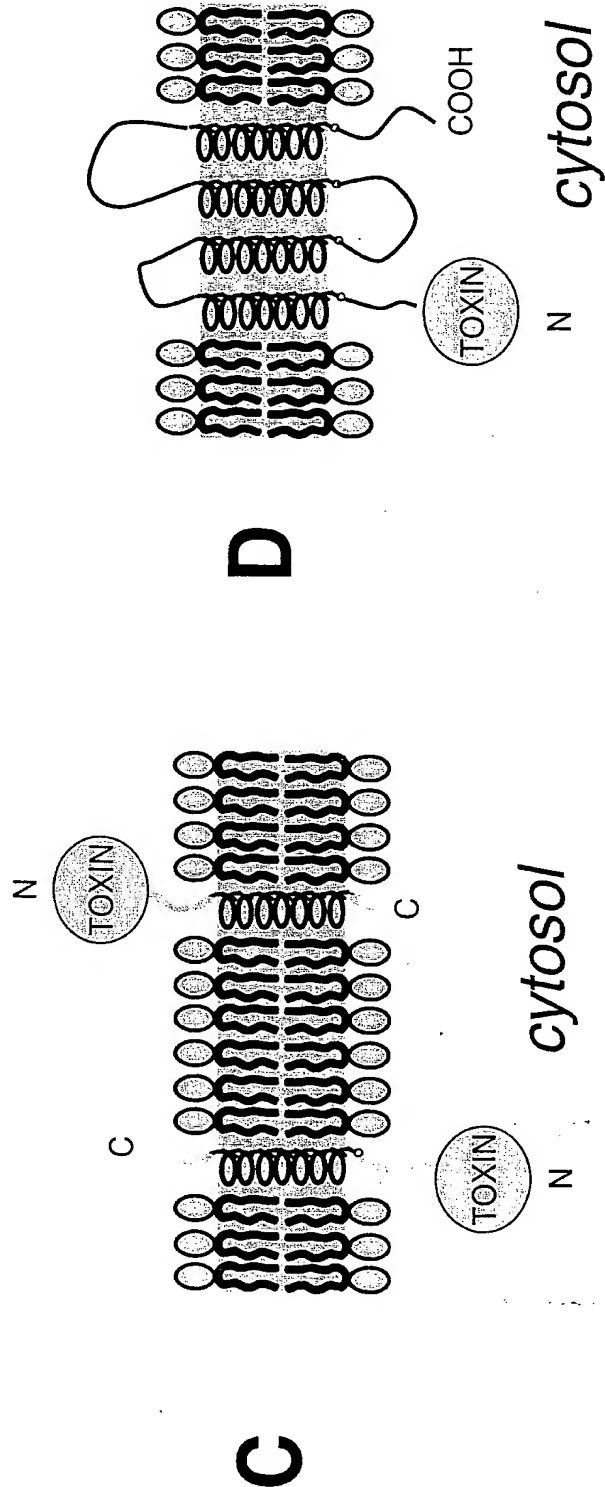
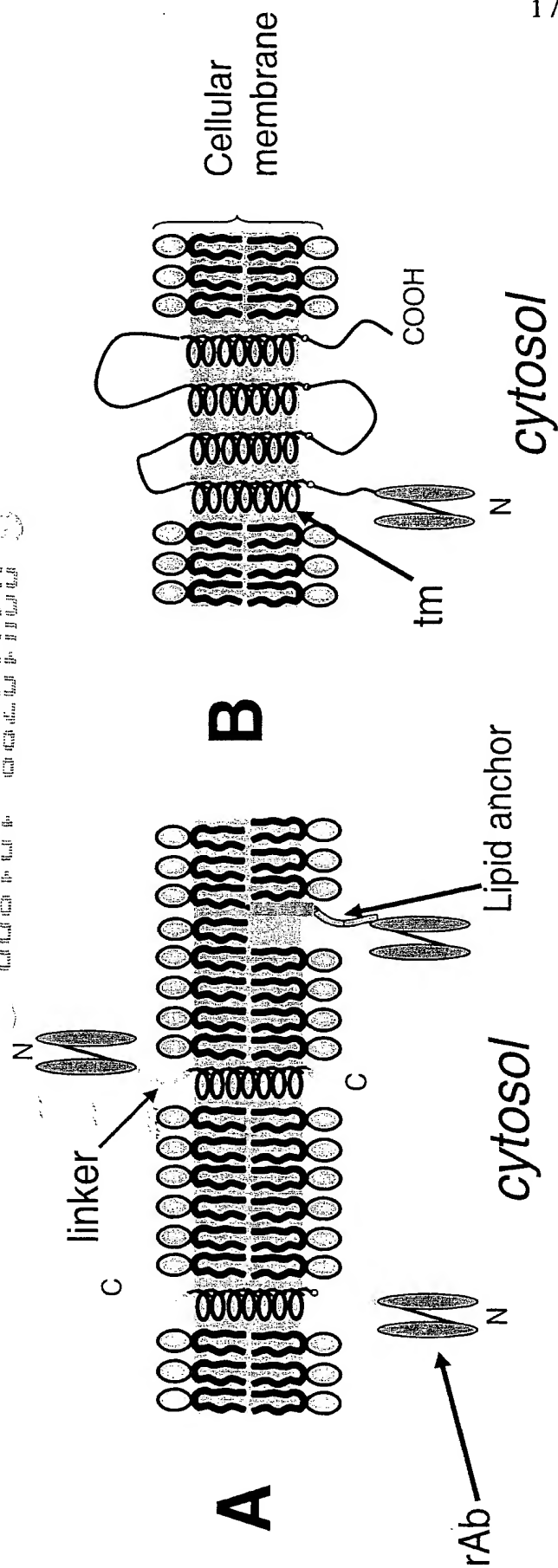


Figure 1

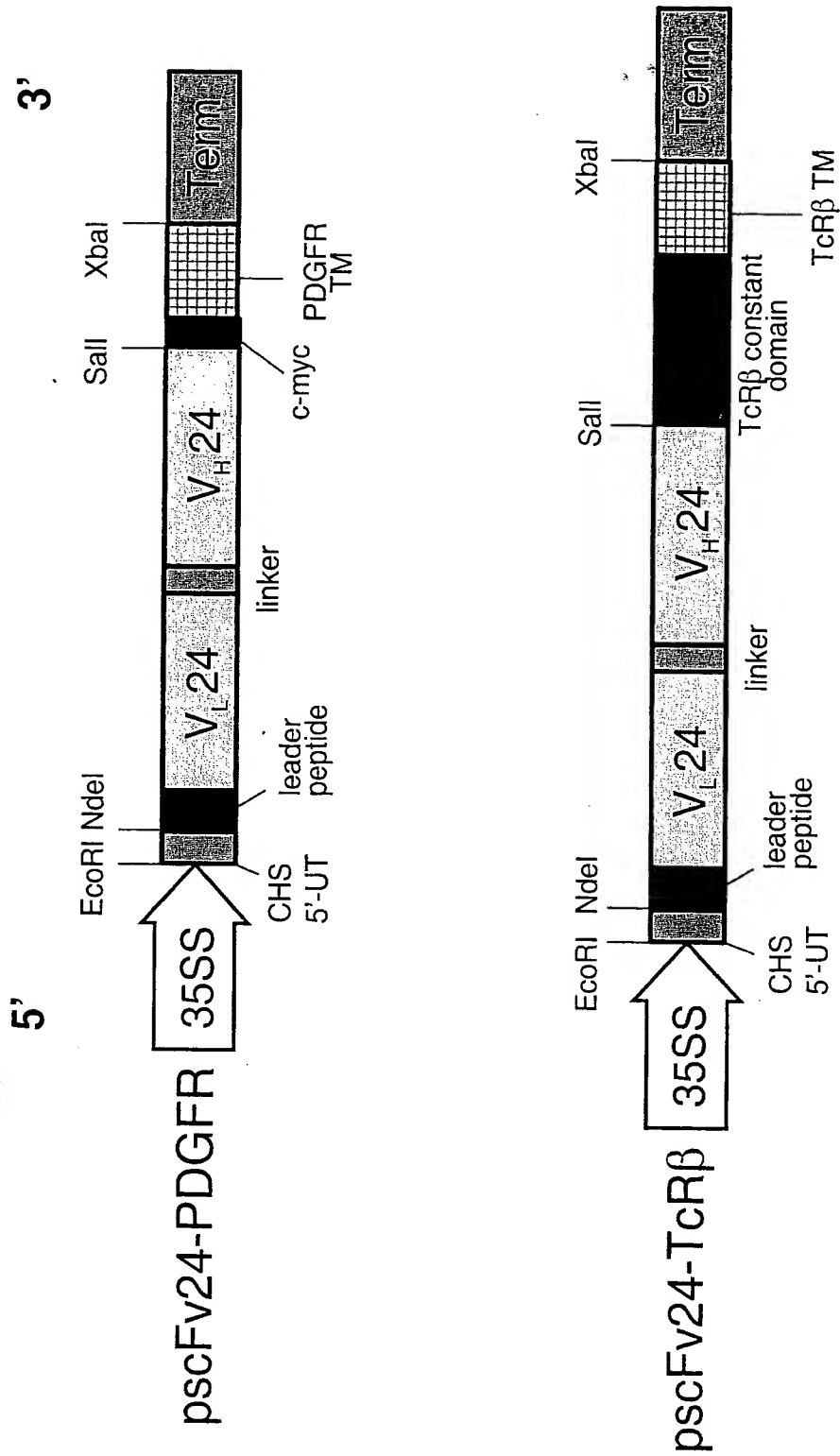


Figure 2

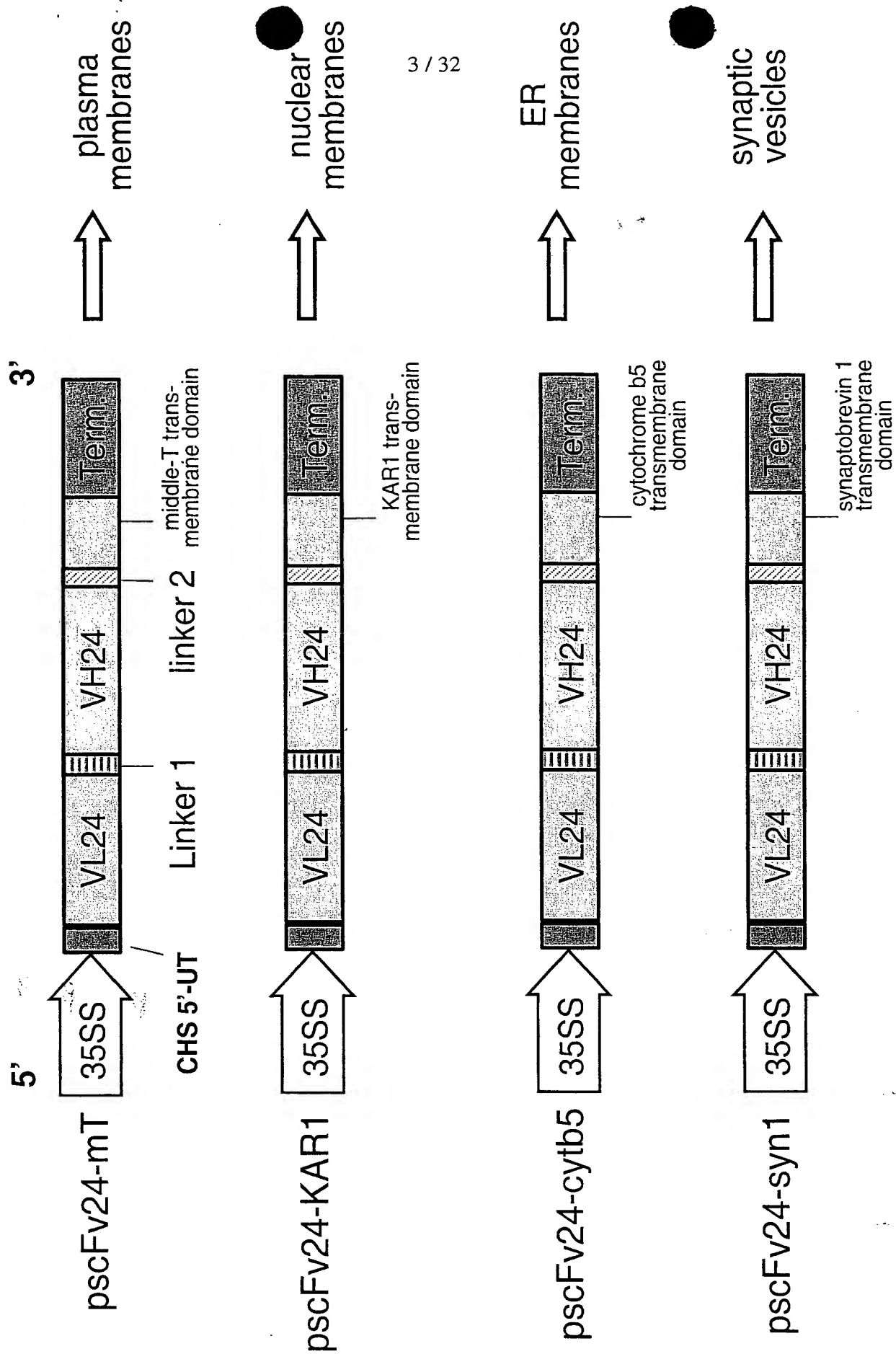


Figure 3

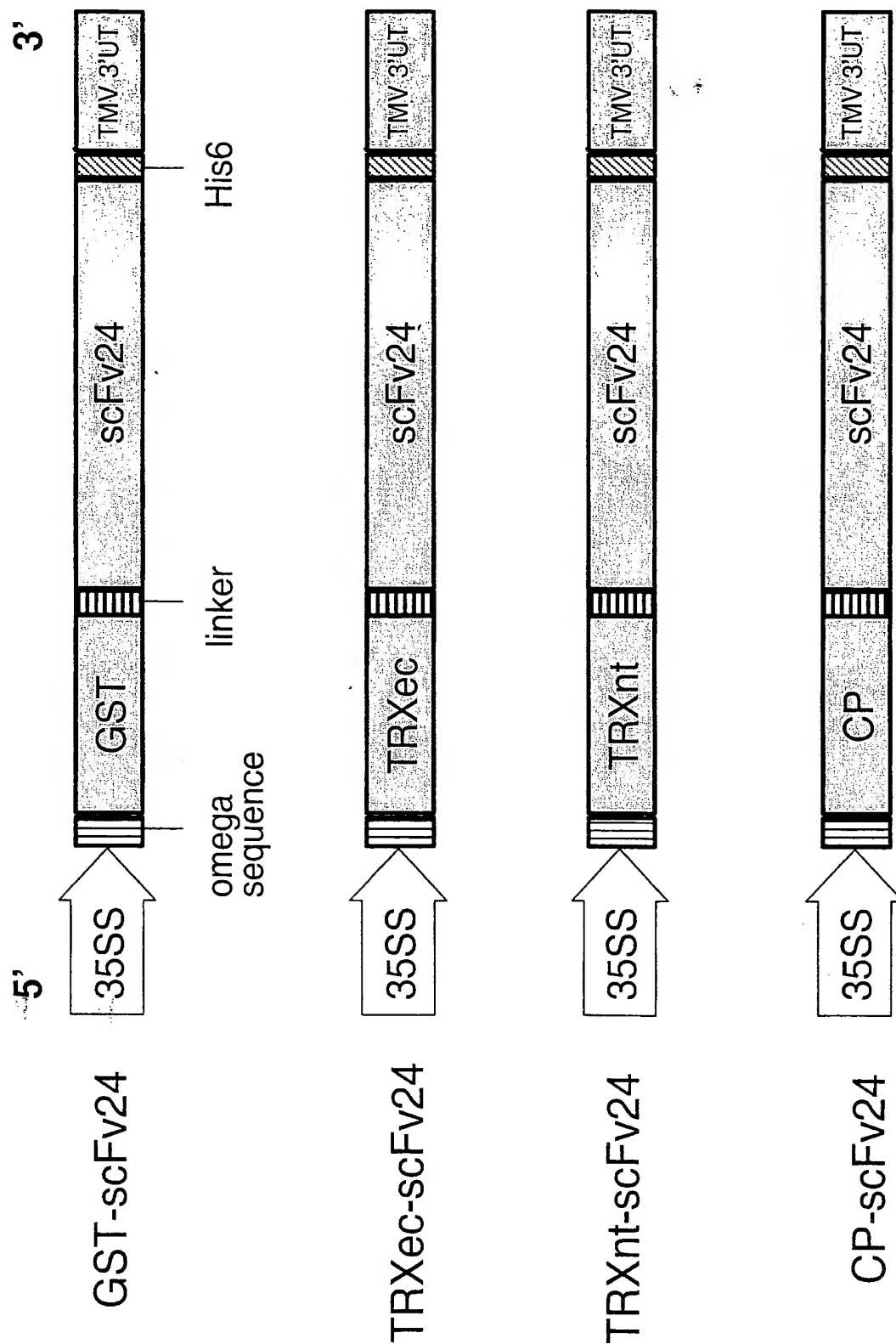
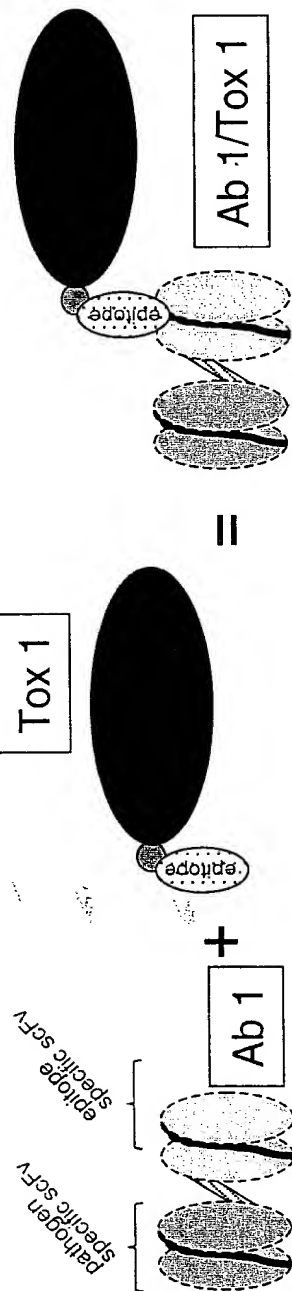
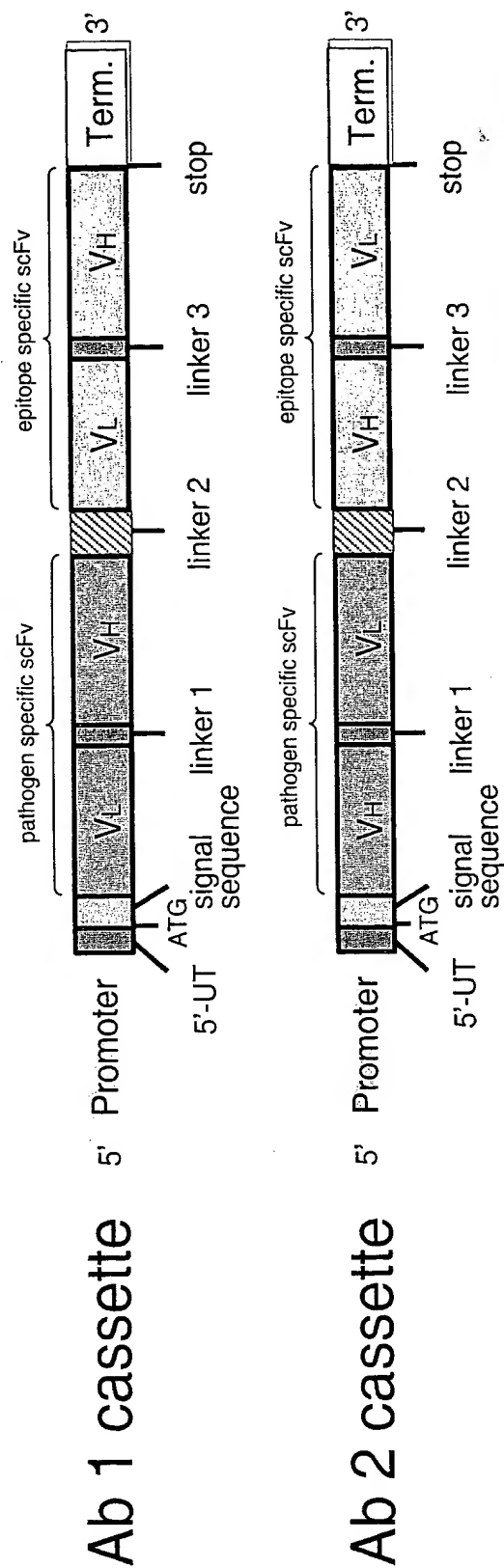


Figure 4

A



B



C

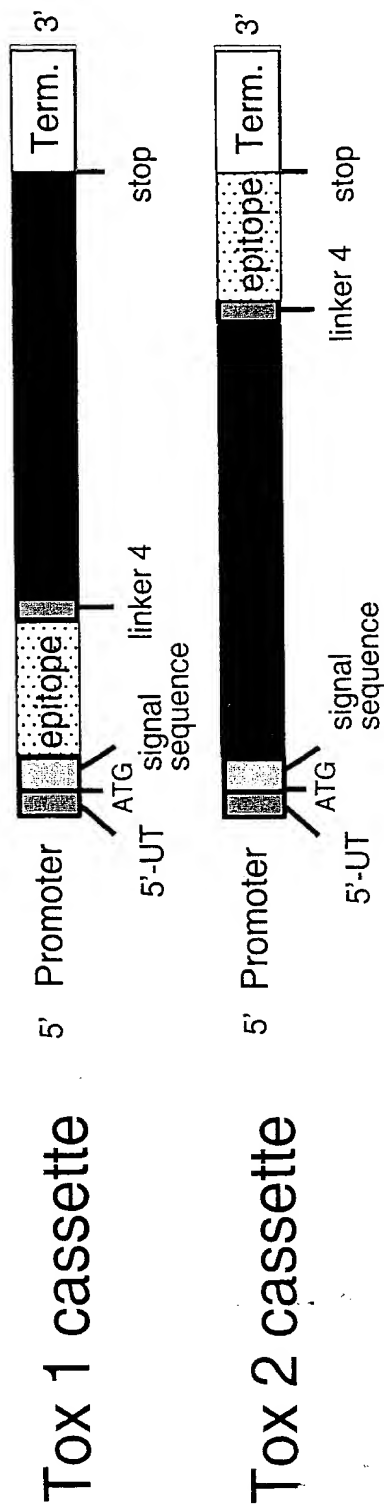


Figure 5

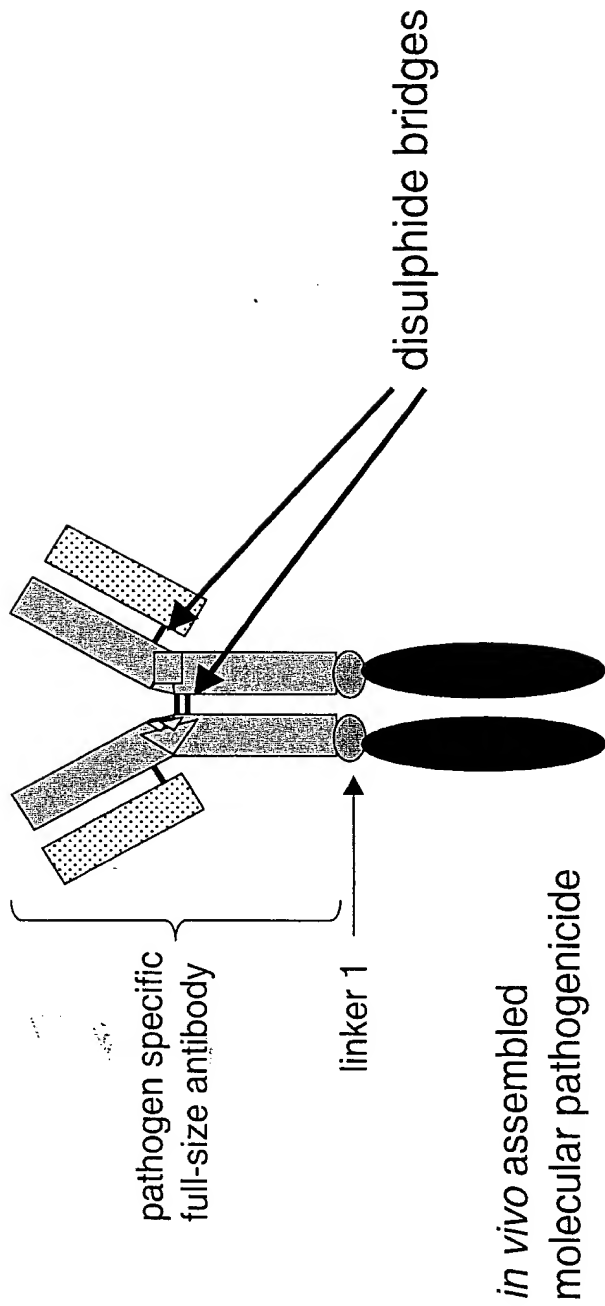
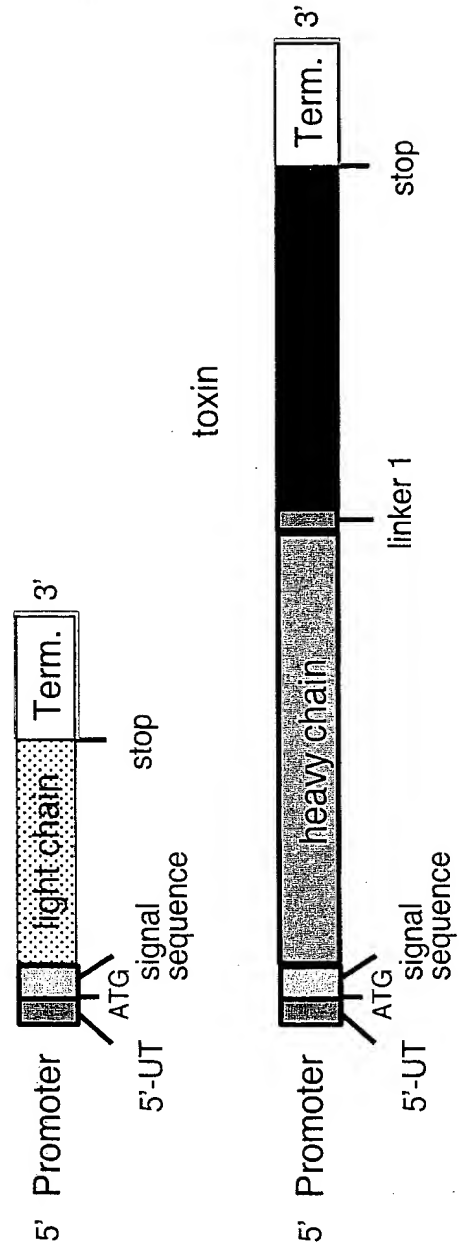
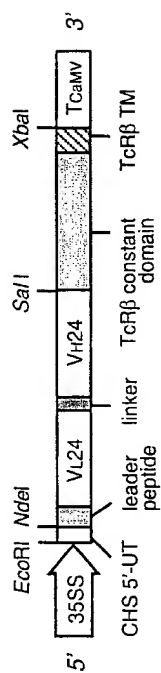
A**B**

Figure 6



pscFv24-TcRβ

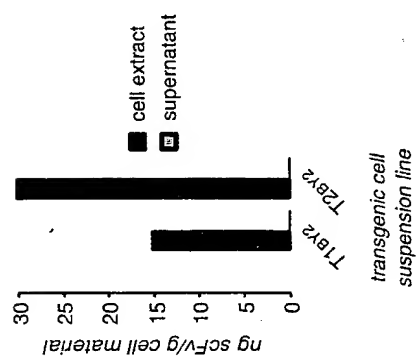
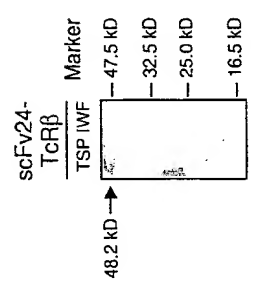


Figure 8



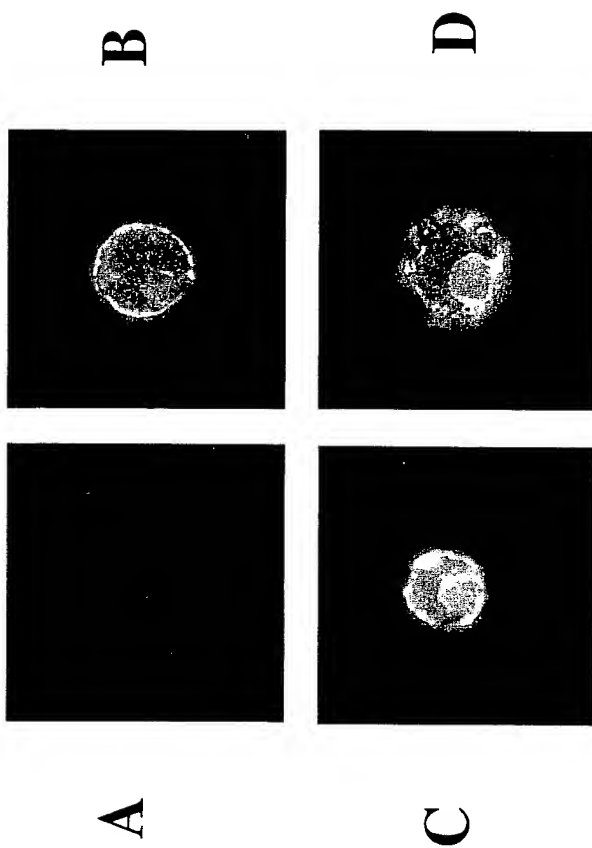


Figure 10

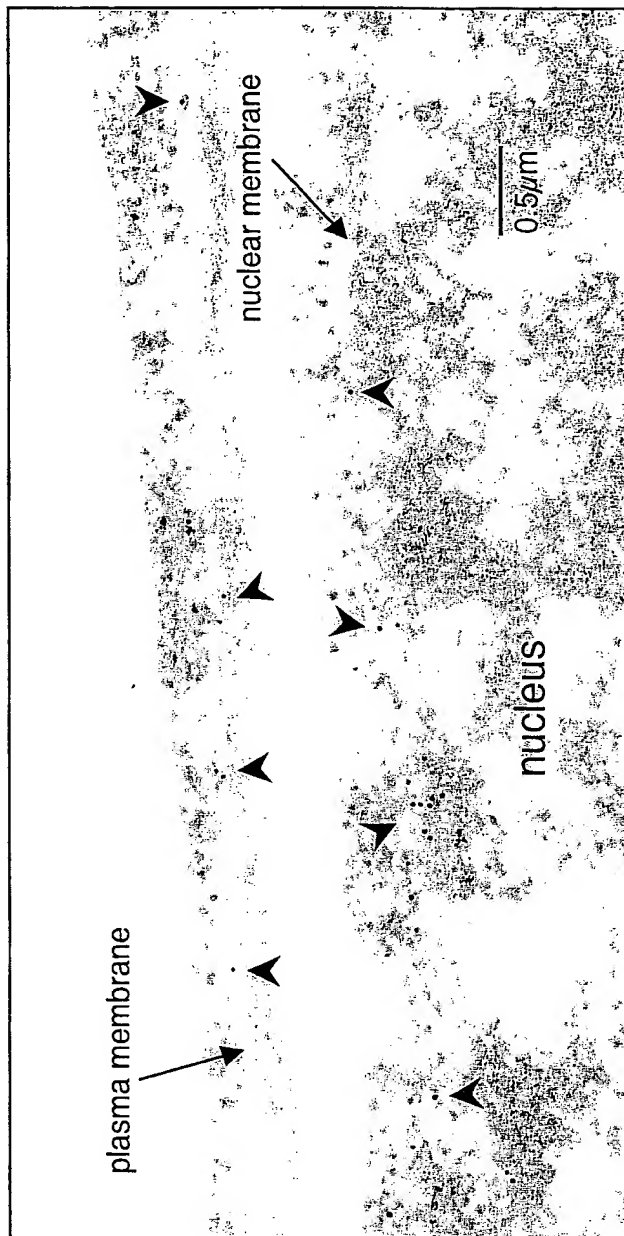


Figure 11

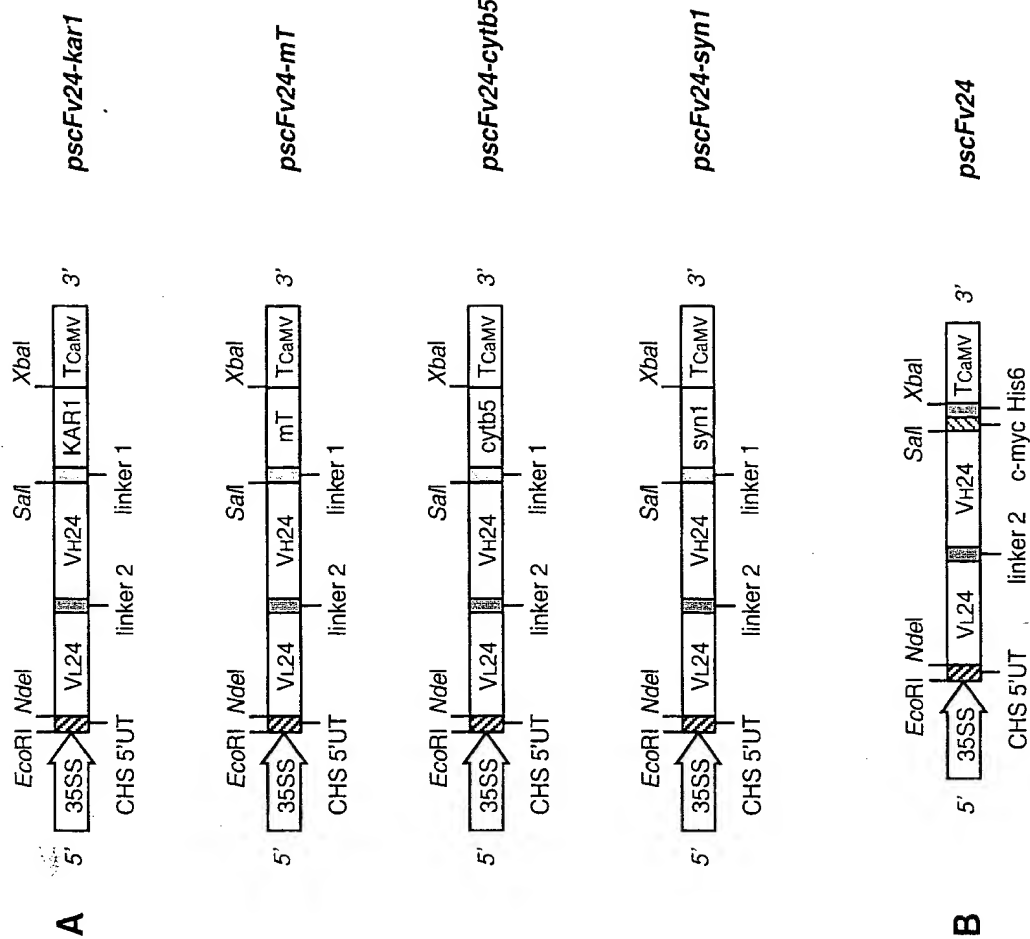
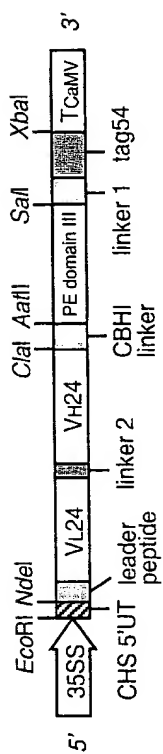


Figure 12



pscFv24-PE400

scFv24 MQIVLTQSPA IMSASPGKEV TMTCSASSSV SKMQWYQOKS GTSPKRWIYD
 Framework I CDR LI Framework II

scFv24 PSKLASGVPG RFSGSGSGTS YSLTISSMEA EDAATYYCOC WSSNPLTFGA
 CDR LII Framework III CDR LIII

scFv24 GTKLEIKGST SGSGKSSEGR GEVQLQQSGP ELVNPGASVK MSCKASGYTF
 Framework IV Linker 212 Framework I

scFv24 PTVVMHWVKQ KPGQGLEWIG YINPNKDGT ENEKFKGKAT LTSDKSSNTA
 CDR LI Framework II CDR LII Framework III

scFv24 YMELSSLTSE DSAVYYCAR VDYDWEAYWG QGTLVTVSAV DGGGSMKRML
 Framework III CDR LIII Framework IV linker RNase

RnaseE INATOOEELR VALVDGORLY DLDIESPGHE OKKANIYKKG ITRIEPSLEA
E. coli RNase E gene --->

RnaseE AFVDYGAERH GFLPLKEIAR EYFPANYSAH GRPNIKDVLR EGOEIVVOID

RnaseE KEERGNGKGA LTTFISLAGS YLVLMNNPR AGGISRRIEG DDRTELKEAL

RnaseE ASLELPEGMG LIVRTAGVGK SAAALOWDLS FRLKHWEAIK KAAESRPAPF

RnaseE LIHOESNVIV RAFRDYLROD IGEILIDNPK VLELAROHIA ALGRPDFSSK

RnaseE IKLYTGEIPL FSHYOIESOI ESAFOREVRL PSGGSIVIDS TEALTAIDIN

RnaseE SARATRGGDI EETAFNTNLE AADEIAROLR LRDLGGLIVI DFIDMTPVRH

RnaseE ORAVENRLRE AVRODRARIO ISHISRFGLL EMSRHRLSPS LGESSHHVCP

RnaseE RCSGTGTVRD NESLSLSILR LIEEEALKEN TOEVHAIVPV PIASYLLNEK

RnaseE RSAVNAIETR ODGVRCVIVP NDOMETPHYH VVRVRKGEET PTLSYMLPKL

RnaseE HEEAMALPSE EEFAERKRPE OPALATFAMP DVPPAPTPAE PAAPVAPAP

RnaseE KAAPATPAAP AOPGLLSRFF GALKALFSGG EETKPTEOPA PKAEAKPERO

RnaseE QDRRKPRONN RRDRNERRDT RSERTEGSDN REENRRNRRO AOOOTAETRE

RnaseE SROQAEVTEK ARTADEOOAP RRERSRRRND DKROAQOEAK ALNVEEOSVO

RnaseE ETEQEERVRP VOPRRKOROL NOKVRYEOSV ABEAVVAPVV EETVAAEPIV

RnaseE QEAPAPRTEL VKVPLPVVAQ TAPEQOEENN ADNRDNGGMP SFSPLASSPA

RnaseE RKWSASSSLS

Fig. 14

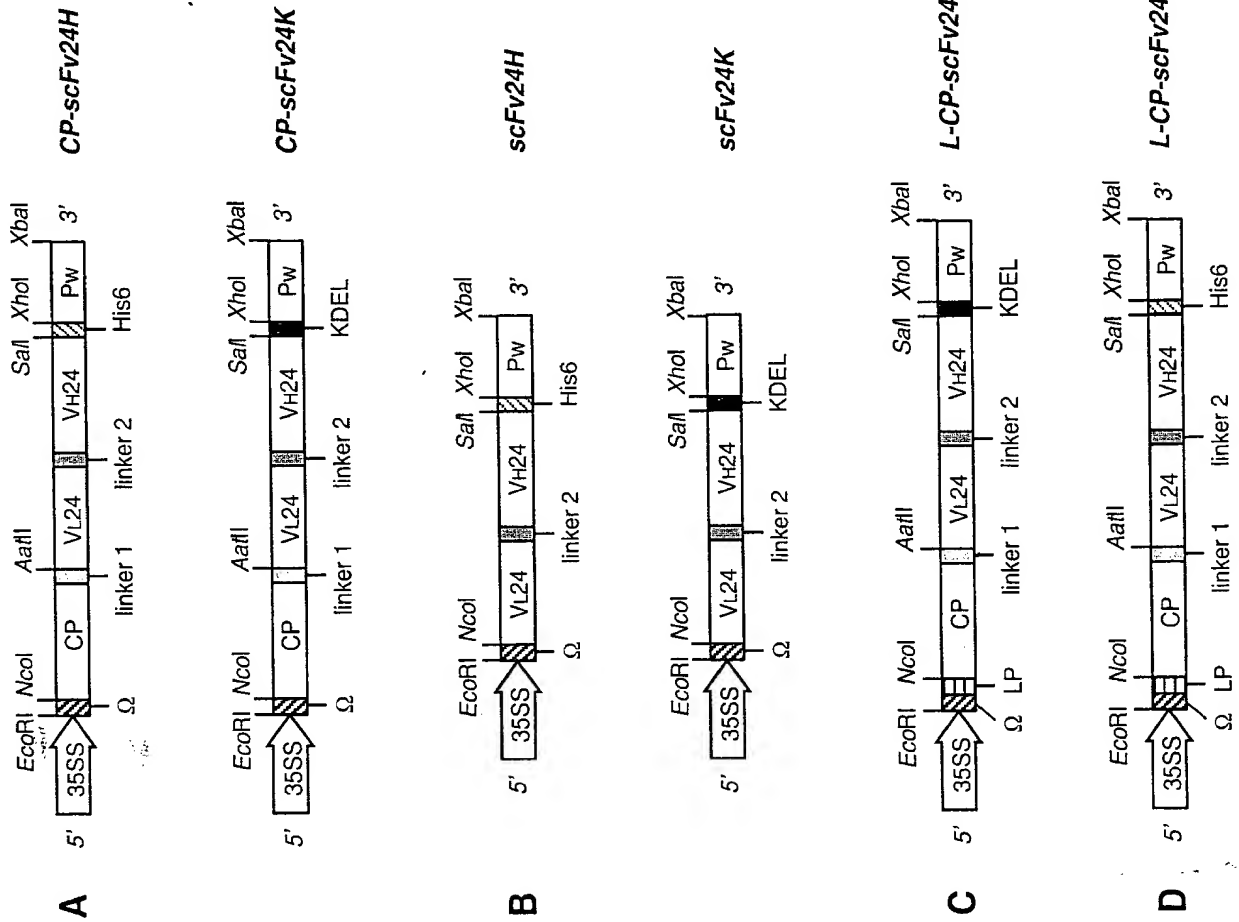


Figure 15

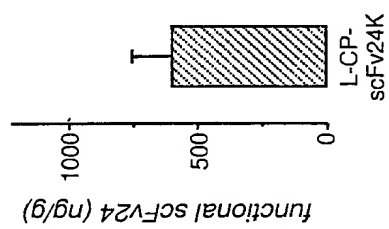


Figure 16

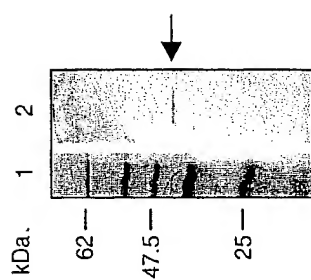


Figure 17

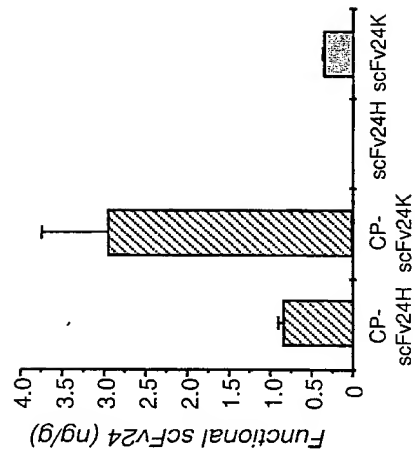


Figure 18

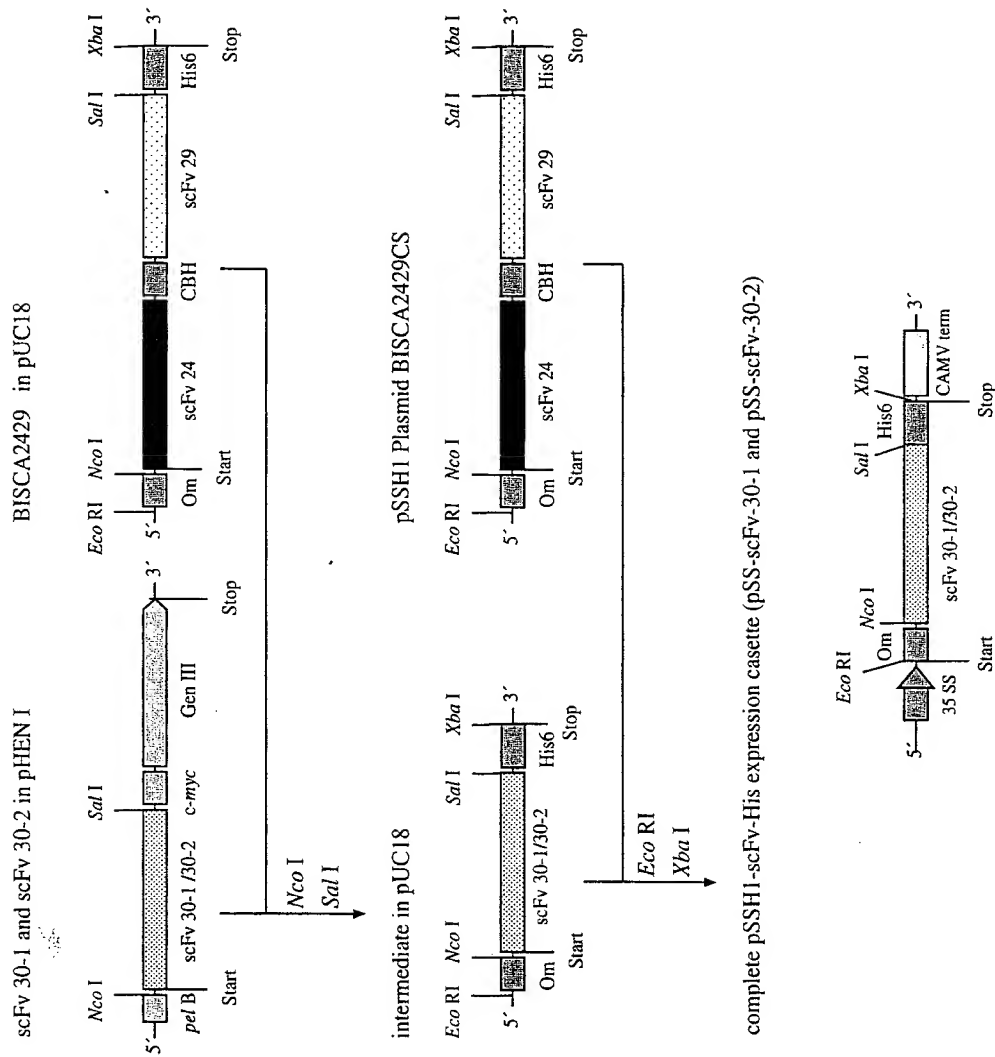


Figure 19

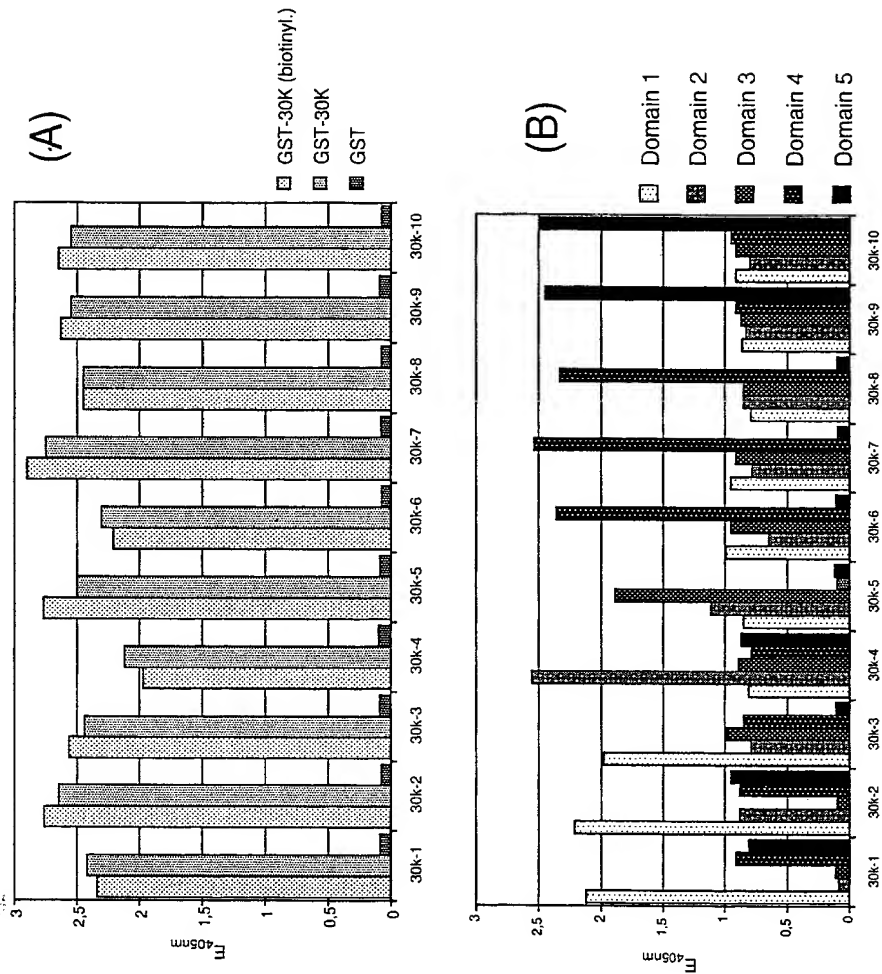


Figure 20

scFv 30-1	--EVHCKQSG	AELVKPGASV	KLSCRASDYT	FTS	WVK	QRPQGGLWEI
scFv 30-2	--EVKLQQSG	AELVKPGASV	KISCKASDYS	FTS	WVK	QSHGKSLEWI
		Framework I		CDR H1		Framework II
scFv 30-1	GEIKPSGNCI	NENEKEKSKA	TLTSDYSSST	AYMQLSSLTS	EDSAVYYCTR	
scFv 30-2	GNEINPMYCSI	SNOKKKKKA	TLTVDKSSST	AYMQLNSLTS	EDSAVYYCAV	
	CDR HII			Framework III		
scFv 30-1	SGNAMD	WGQGTITVTVS	SGGGGSGGGG	SGGGGS	DIVL	TLSPATLSVT
scFv 30-2	SGNAMD	WGQGTITVTVS	SGGGGSGGGG	SGGGGS	DILL	TQSPLSLPVS
	CDR HIII	Framework IV	Linker (Gly ₄ Ser) ₃			
scFv 30-1	PGDRVSLSCR	ASOSTSNLFE	WYQQK	SHESPRLLIK	MSOSTSGIP	
scFv 30-2	LGDHASISCR	SSOSTSVESNC	NVYTHWYLQN	PGQSPKLLIY	KVSNRESGIP	
	Framework I	CDR LI		Framework II	CDR LII	
scFv 30-1	STFSGSGSGT	DFTLSINSVD	TEDFGMYFCG	QSNWPFRFG	SGIKLELKSA	
scFv 30-2	DRFSGSGSGT	DFTLKISRVE	AEDLGVYFCS	QSTHWPFRFG	GGTKLELKRA	
		Framework III		CDR LIII	Framework IV	
scFv 30-1	VDAAAEQKLI	SEEDLNGAA*				
scFv 30-2	VDAAAEQKLI	SEEDLNGAA*				
		c-myc tag				

Fig. 21

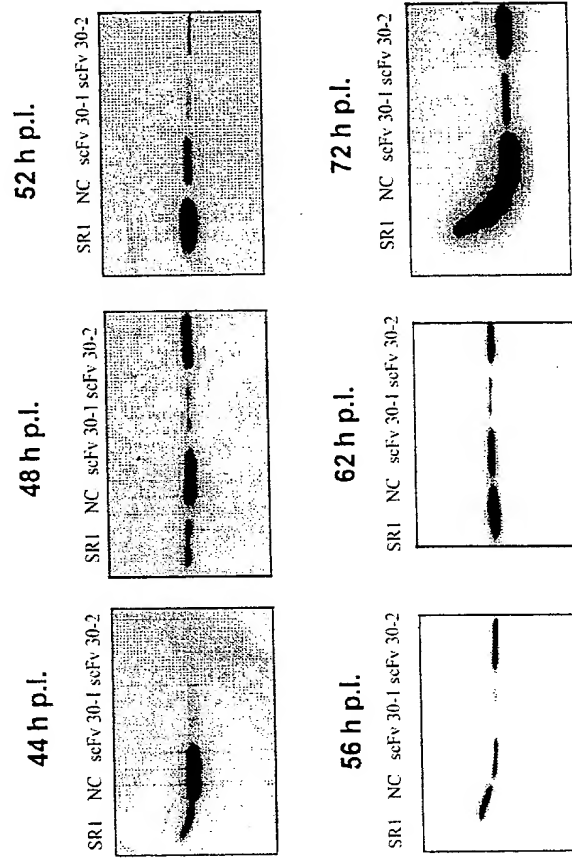


Figure 22

MAEVQLQQSG AELVKPGASV KMSCKASGYT FTNYNMHWVK QTPGQGLEWI
 GAIYPRNGDT SYNQKFKGKA TLTADKSSST AYMQLSSLTS EDSAVYYCAR
 PDVWGAGTLL TVSAGAGPTS GSGKPGPEG STKGAPDVLMTQAPLTLSVT
 IGQPASISCK SSQSLLDGDG KTYLNWLLQR PGQSPKRLIY LVSKLDSGVP
 DRFTGSGSGT DFTLKISRVE AEDLGVYYCW QGTHFPHTFG GGTKLEIKRA
 RAVDAAA

Figure 23a: Aminoacid sequence of scFv - 3a-2 derived from cDNA

MAQVTLKESG PGILKPSQTL SLTCSFSGFS LSTSGMGVGW IRQPSGKGLE
 WLAHIWWDDD KYYNPSLRSQ LTISKDTSRN QVFLRITNVD TADTATYYCA
 RGYYGNDSPF AYWGQGTLLT VSSGAGPTSG SGKPGPEGSTKGAPDIVLS
 QSPKFMSTSV GDRVSITCKA SQIVRTAVAW FQKPGQSPK ALIYLASNRH
 TGVDPDRFTGS GSGTDFTLTI SNVQSEDLAD YFCLQHWNYF FTFGSGTKLE
 IKRAVDAAA

Figure 23b: Aminoacid sequence of scFv 54-1 derived from cDNA

MAQIQLVQSG PELKKPGQTV KISCKASAYT FTDYSMHWVK QAPGKGLKWM
 GWINTETGEP TYADDFKGRF AFSLETSAST AYLQINTLKN EDSATYFCAR
 GSGFNPHYWGQ GTLVTVSAGA GPTSGSGKPG PEGSGTKGAP DIVLSQSPSS
 LAVSVGEKVT MSCKSSQSLL YSSNQKNYLA WYQKPGQSP KLLIYWASTR
 ESGVPDRFTG SSGTDFTLTI INSVKAEDLA VYYCQYYSY VTFGAGTKLE
 IKRAVDAAA

Figure 23c: Aminoacid sequence of scFv - 3min derived from cDNA

Fig. 23

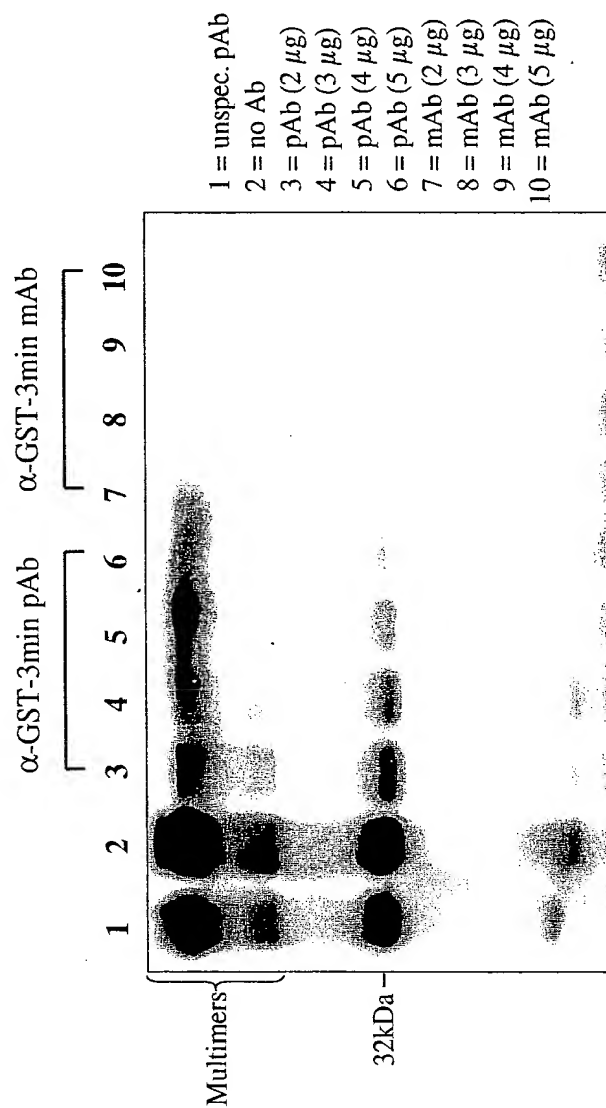


Figure 24

(a) TMV-coatprotein:

127 128 129 130 131 132 133 134 135 136 137 138
N L I V E L I R G T G S

pVIII 9aa:

A1: K T D L V C R A T
A2: R I V I C G R V T
A4: R G T L P A R G T
A5: V G R Q R D T Q S
B5: F L R V D A R E T
C4: V A G M L G K G T
D5: R W E L A N R S T
E5: P S A L G T R E T
F3: K N D L V S R A T
G1: Q I V S A W R E T

pVIII 9aa.Cys:

B9/G1: C A L P A R H I G R C
F3: C Q L P A R A T S S C
H1: C I T S Q R E T G W C
H5: C R R S T T G I C
H10: C S T T L Y K R G T C

consensus-sequence:

R V D L P A R E T

(b) 54K-protein:

402 403 404 405 406 407 408 409 410 411 412 413
K H I K D W E H L E E F

A2/A9/B8/C9: K R K D G E H W L
A6/B5/F8/H1: R Q A K S W S S L
G5: Y Q A K E W S N L
H10: K D W E H R V P S

consensus-sequence:

K D W E/S H L

(c) GST-3min:

← GST ———— 3min ———→
-6 -5 -4 -3 -2 -1 +1 +2 +3 +4 +5 +6
P K S D P Q M G K R R R

pVIII 9aa:

A8: H P R P Q L A S L
C2: H P D P Q S S H S
E7: R F T D P Q L H P
F5: K Q D P Q Q Q K Q
F8: V P D S Q Q L E W P
G7: H C D P Q L Y Q E
H1: D P Q M F R R H C
H5: F K D G Q L R P Q

pVIII 9aa.Cys:

A4: C P D P Q L R L H R C
A5: C P D P Q L N G T R C
A7/B10/H4: C P D P Q L S S L R C
A8: C P D P Q L R L H R C
A9: C P D P Q L T L H R C
G4: C P D P Q L S L Q R C
H6: C P D A Q L S G T R C

consensus-sequence:

H P D P Q L S L H R

Fig. 25

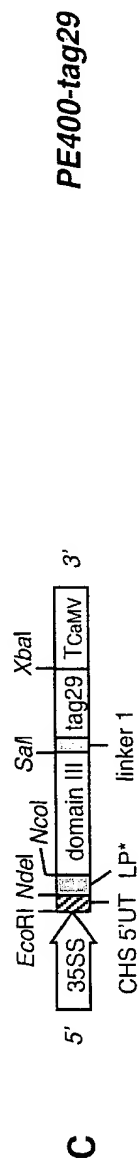
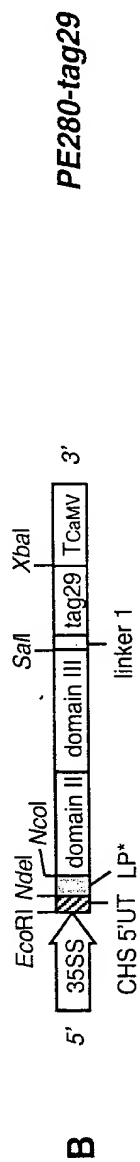
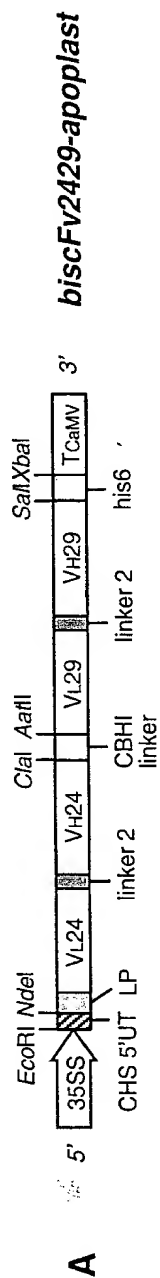


Figure 26

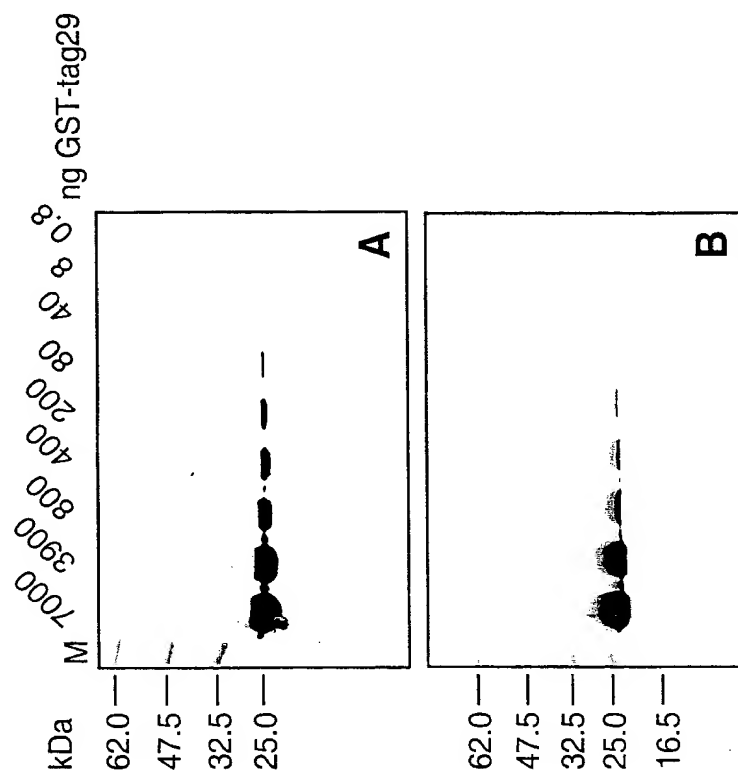


Figure 27

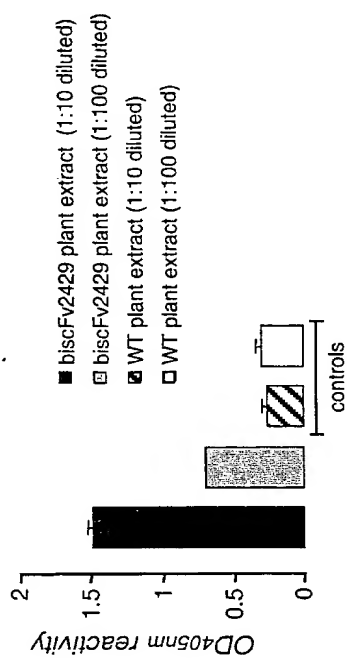


Figure 28

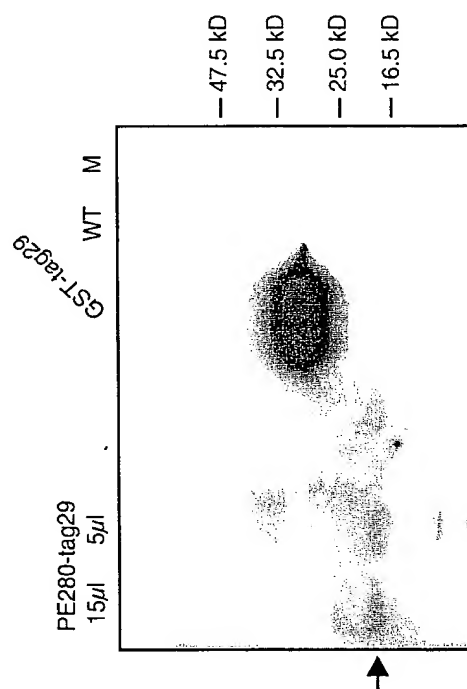
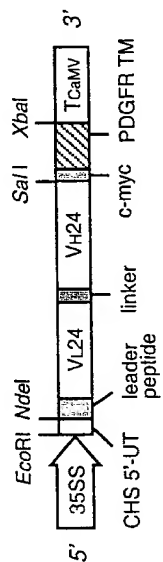


Figure 29



pscFv24-PDGFR

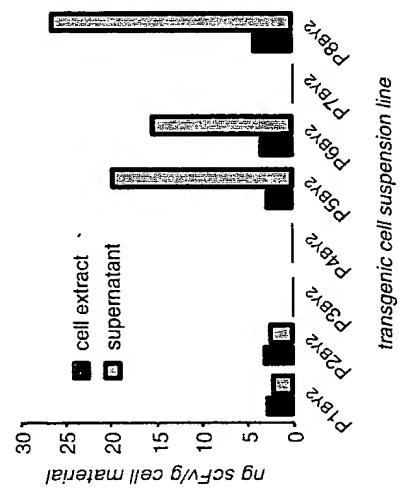


Figure 31

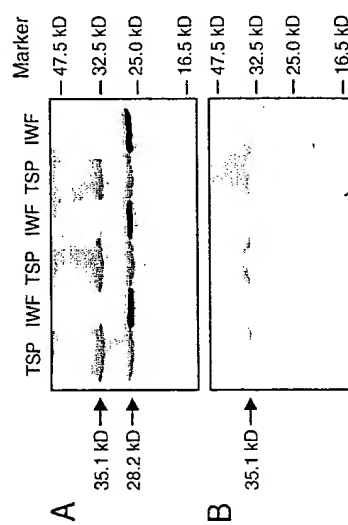


Figure 32